**What is claimed is:**

1. A method of assessing a combinatorial library for complementarity to a target having at least one binding site, said combinatorial library comprising a plurality of ligands, each based on a common core, said method comprising:

docking each ligand of the plurality of ligands to the target molecule to generate a plurality of ligand positions relative to the target molecule in a plurality of ligand-target molecule complex formations, said plurality of ligand positions comprising a plurality of common core positions relative to the target molecule;

determining an rms deviation of each common core position of said plurality of common core positions from other common core positions; and

forming clusters according to said rms deviation.

2. A method according to claim 1, additionally comprising rating complementarity of the combinatorial library to the target molecule according to number of ligands in a cluster having a minimum rms deviation relative to number of ligands in the combinatorial library.

3. A method according to claim 1 wherein said determining an rms deviation comprises:

placing a grid around a binding site of the target molecule;

for each ligand position, determining a location on the grid corresponding to the center of mass of the common core; and

determining the rms deviation of each common core position from every other common core position having a location on the grid within a predetermined distance.

4. A method according to claim 1 wherein said forming clusters comprises forming clusters using a single linkage clustering algorithm.

5. A method according to claim 1 wherein said docking each ligand comprises:

performing a pre-docking conformational search to generate multiple solution conformations of each ligand;

generating a binding site image of the target molecule, said binding site image comprising multiple hot spots;

matching hot spots of the binding site image to atoms in at least one solution conformation of the multiple solution conformations of each ligand to obtain at least one ligand position relative to the target molecule in a ligand-target molecule complex formation; and

optimizing the at least one ligand position while allowing translation, orientation and rotatable bonds of the ligand to vary, and while holding the target molecule fixed.

6. A system for assessing a combinatorial library for complementarity to a target having at least one binding site, said combinatorial library comprising a plurality of ligands, each based on a common core, said system comprising:

means for docking each ligand of the plurality of ligands to the target molecule to generate a plurality of ligand positions relative to the target molecule in a plurality of ligand-target molecule complex formations, said plurality of ligand positions comprising a plurality of common core positions relative to the target molecule;

means for determining an rms deviation of each common core position of said plurality of common core positions from other common core positions; and

means for forming clusters according to said rms deviation.

7. A system according to claim 1, additionally comprising means for rating complementarity of the combinatorial library to the target molecule according to number of ligands in a cluster having a minimum rms deviation relative to number of ligands in the combinatorial library.

8. A system according to claim 1 wherein said means for determining an rms deviation comprises:

means for placing a grid around a binding site of the target molecule;

means for, for each ligand position, determining a location on the grid corresponding to the center of mass of the common core; and

means for determining the rms deviation of each common core position from every other common core position having a location on the grid within a predetermined distance.

9. A system according to claim 1 wherein said means for forming clusters comprises means for forming clusters using a single linkage clustering algorithm.

10. A system according to claim 1 wherein said means for docking each ligand comprises:

means for performing a pre-docking conformational search to generate multiple solution conformations of each ligand;

means for generating a binding site image of the target molecule, said binding site image comprising multiple hot spots;

means for matching hot spots of the binding site image to atoms in at least one solution conformation of the multiple solution conformations of each ligand to obtain at least one ligand position relative to the target molecule in a ligand-target molecule complex formation; and

means for optimizing the at least one ligand position while allowing translation, orientation and rotatable bonds of the ligand to vary, and while holding the target molecule fixed.

11. At least one program storage device readable by a machine, tangibly embodying at least one program of instructions executable by the machine to perform a method for assessing a combinatorial library for complementarity to a target having at least one binding site, said combinatorial library comprising a plurality of ligands, each based on a common core, said method comprising:

docking each ligand of the plurality of ligands to the target molecule to generate a plurality of ligand positions relative to the target molecule in a plurality of ligand-target molecule complex formations, said plurality of ligand positions comprising a plurality of common core positions relative to the target molecule;

determining an rms deviation of each common core position of said plurality of common core positions from other common core positions; and

forming clusters according to said rms deviation.

12. The at least one program storage device according to claim 1, wherein said method additionally comprises rating complementarity of the combinatorial library to the target molecule according to number of ligands in a cluster having a minimum rms deviation relative to number of ligands in the combinatorial library.

13. The at least one program storage device according to claim 1, wherein said determining an rms deviation comprises:

placing a grid around a binding site of the target molecule;

for each ligand position, determining a location on the grid corresponding to the center of mass of the common core; and

determining the rms deviation of each common core position from every other common core position having a location on the grid within a predetermined distance.

14. The at least one program storage device according to claim 1, wherein said forming clusters comprises forming clusters using a single linkage clustering algorithm.

15. The at least one program storage device according to claim 1, wherein said docking each ligand comprises:

performing a pre-docking conformational search to generate multiple solution conformations of each ligand;

generating a binding site image of the target molecule, said binding site image comprising multiple hot spots;

matching hot spots of the binding site image to atoms in at least one solution conformation of the multiple solution conformations of each ligand to obtain at least one ligand position relative to the target molecule in a ligand-target molecule complex formation; and

optimizing the at least one ligand position while allowing translation, orientation and rotatable bonds of the ligand to vary, and while holding the target molecule fixed.